RAW SEQUENCE LISTING   DATE: 05/23/2000
PATENT APPLICATION: US/09/225,502A   TIME: 21:22:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05232000\I225502A.raw

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 3 <110> APPLICANT: Moore et al.
 5 <120> TITLE OF INVENTION: Human FK506 Binding Proteins
 7 <130> FILE REFERENCE: PF392
 9 <140> CURRENT APPLICATION NUMBER: 09/225,502A
10 <141> CURRENT FILING DATE: 1999-01-06
12 <150> PRIOR APPLICATION NUMBER: 60/070,875
13 <151> PRIOR FILING DATE: 1998-01-09
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1234
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (61)..(1071)
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32 Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
33   1               5                  10                  15
35 ctg cag ttg ctg cta ctg gtg gtg cag gcc gtg ggg agg ggg ctg ggc  156
36 Leu Gln Leu Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
37              20                  25                  30
39 cgc gcc agc ccg gcc ggg ggc ccc ctg gaa gat gtg gtc atc gag agg  204
40 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
41          35                  40                  45
43 tac cac atc ccc agg gcc tgt ccc cgg gaa gtg cag atg ggg gat ttt  252
44 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
45      50                  55                  60
47 gtg cgc tac cac tac aac ggc act ttt gaa gat ggc aag aag ttt gat  300
48 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
49  65                  70                  75                  80
51 tca agc tat gat cgc aac acc ttg gtg gcc atc gtg gtg ggt gtg ggg  348
52 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
53                  85                  90                  95
55 cgc ctc atc act ggc atg gac cga ggc ctc atg ggc atg tgt gtc aac  396
56 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
57              100                 105                 110
59 gag cgg cga cgc ctc att gtg cct ccc cac ctg ggc tat ggg agc atc  444
60 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
61          115                 120                 125
63 ggc ctg gcg ggg ctc att cca ccg gat gcc acc ctc tac ttc gat gtg  492
64 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
65      130                 135                 140
67 gtt ctg ctg gat gtg tgg aac aag gaa gac acc gtg cag gtg agc aca  540
68 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
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69 145                150                155                160
71 ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac ggc gac ttt   588
72 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
73                165                170                175
75 gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc tcc ttc gac   636
76 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
77                180                185                190
79 acc agc tac agt aag ggc ggc act tat gac acc tac gtc ggc tct ggt   684
80 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
81          195                200                205
83 tgg ctg atc aag ggc atg gac cag ggg ctg ctg ggc atg tgt cct gga   732
84 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
85      210                215                220
87 cag aga agg aag att atc atc cct cca ttc ctg gcc tat ggc gag aaa   780
88 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
89 225                230                235                240
91 ggc tat ggt gag ggt ggg caa gga cac aag ggg aaa ttc cgc aga aga   828
92 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
93                245                250                255
95 ggg aaa aac cag gcc tcc aca tac agt tgc tca ggt tgt ata ctg cac   876
96 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
97          260                265                270
99 gag ggc atc caa cca agg act caa ggt ggg atg aaa tct acc ctt ggt   924
100 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
101          275                280                285
103 gct act aag aag ggg tgc ttt ggc cgg gcg tgg tgg ctc acg ctt gta   972
104 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
105      290                295                300
107 atc cca gca ctt tgg gaa gcc aag gcg gga gga tca cga ggt cca gga   1020
108 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser Arg Gly Pro Gly
109 305                310                315                320
111 gat cga gac cac ggt gaa acc ccg tct cta cta aaa ata caa aaa aat   1068
112 Asp Arg Asp His Gly Glu Thr Pro Ser Leu Leu Lys Ile Gln Lys Asn
113                325                330                335
115 tag ccgggcgtgg tgggggcgcc tgtagtccca gctactcgga gaggctgagg       1121
118 caggaaaatg acgtgaaccc gggaggcgga gcttgcagtg agccgagatc ttgccactgc 1181
120 actccagcct gggtgacaga gcgagactct gtctcaaaaa aaaaaaaaa aaa         1234
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124 <211> LENGTH: 336
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 2
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130 1               5                  10                 15
131 Leu Gln Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
132               20                 25                 30
133 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
134          35                 40                 45
135 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
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PATENT APPLICATION: US/09/225,502A   TIME: 21:22:02

Input Set : A:\Pto.amc
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136      50                   55                 60
137 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
138 65                   70                 75                 80
139 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
140                 85                 90                 95
141 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
142                100                105                110
143 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
144         115                120                125
145 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
146         130                135                140
147 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
148 145                 150                155                160
149 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
150                165                170                175
151 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
152                180                185                190
153 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
154         195                200                205
155 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
156         210                215                220
157 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
158 225                 230                235                240
159 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
160                245                250                255
161 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
162                260                265                270
163 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
164         275                280                285
165 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
166         290                295                300
167 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser Arg Gly Pro Gly
168 305                 310                315                320
169 Asp Arg Asp His Gly Glu Thr Pro Ser Leu Leu Lys Ile Gln Lys Asn
170                325                330                335
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 2145
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapiens
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (2)..(1324)
183 <400> SEQUENCE: 3
184 c ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac acc gtg cag  49
185   Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln
186   1               5                  10                 15
188 gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac  97
189 Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp
190                20                 25                 30
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RAW SEQUENCE LISTING   DATE: 05/23/2000
PATENT APPLICATION: US/09/225,502A   TIME: 21:22:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05232000\I225502A.raw

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192 ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc   145
193 Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr
194         35                  40                  45
196 tcc ttc gac acc agc tac agt aag ggc ggc act tat gac acc tac gtc   193
197 Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val
198     50                  55                  60
200 ggc tct ggt tgg ctg atc aag ggc atg gac cag ggg ctg ctg ggc atg   241
201 Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met
202 65                  70                  75                  80
204 tgt cct gga gag aga agg aag att atc atc cca ttc ctg gcc tat       289
205 Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr
206                 85                  90                  95
208 ggc gag aaa ggc tat ggg aca gtg atc ccc cca cag gcc tcg ctg gtc   337
209 Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val
210         100                 105                 110
212 ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac gct gtc cag   385
213 Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln
214         115                 120                 125
216 cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga gcc ggg gcc   433
217 Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala
218     130                 135                 140
220 ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg gac ggc acc   481
221 Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr
222 145                 150                 155                 160
224 ctc ttc gat tcc agc tac tcc cac aac cac acc tac aat acc tat atc   529
225 Leu Phe Asp Ser Ser Tyr Ser His Asn His Thr Tyr Asn Thr Tyr Ile
226                 165                 170                 175
228 ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg cag ggt gcc   577
229 Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala
230             180                 185                 190
232 tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac ctc gcc tat   625
233 Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr
234         195                 200                 205
236 ggg gag aat gga act gga gac aag atc cct ggc tct gcc gtg cta atc   673
237 Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile
238     210                 215                 220
240 ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat gtg gtg gaa   721
241 Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu
242 225                 230                 235                 240
244 atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag acc acc aag   769
245 Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu Thr Thr Lys
246             245                 250                 255
248 ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg ctg gac ggc   817
249 Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly
250             260                 265                 270
252 acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag gag gcg act   865
253 Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr
254     275                 280                 285
256 ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc ctg cag ggc   913
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                    RAW SEQUENCE LISTING            DATE: 05/23/2000
                    PATENT APPLICATION:  US/09/225,502A    TIME: 21:22:02

                    Input Set : A:\Pto.amc
                    Output Set: N:\CRF3\05232000\I225502A.raw

257 Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly
258     290             295             300
260 atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg cac ctg gcc   961
261 Met Cys Val Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala
262 305             310             315             320
264 cac ggg gag agt gga gcc cgg gga gtc cca ggc agt gct gtg ctg ctg  1009
265 His Gly Glu Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu
266             325             330             335
268 ttt gag gtg gag ctg gtg tcc cgg gag gat ggg ctg ccc aca ggc tac  1057
269 Phe Glu Val Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr
270             340             345             350
272 ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt gaa gac ata  1105
273 Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Ile
274         355             360             365
276 gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc tcc acc ttc  1153
277 Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe
278     370             375             380
280 atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg cct ggg cag  1201
281 Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln
282 385             390             395             400
284 gac cct gag aaa acc ata gga gac atg ttc cag aac cag gac cgc aac  1249
285 Asp Pro Glu Lys Thr Ile Gly Asp Met Phe Gln Asn Gln Asp Arg Asn
286             405             410             415
288 cag gac ggc aag atc aca gtc gac gag ctc aag ctg aag tca gat gag  1297
289 Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu
290             420             425             430
292 gac gag gag cgg gtc cac gag gag ctc tgagggcag ggagcctggc          1344
293 Asp Glu Glu Arg Val His Glu Glu Leu
294             435             440
296 caggcctgag acacagaggc ccactgcgag ggggacagtg gcggtgggac tgacctgctg 1404
298 acagtcaccc tccctctgct gggatgaggt ccaggagcca actaaaacaa tggcagagga 1464
300 gacatctctg gtgttccac  caccctagat gaaaatccac agcacagacc tctaccgtgt 1524
302 ttctcttcca tccctaaacc acttccttaa aatgtttgga tttgcaaagc caatttgggg 1584
304 cctgtggagc ctgggtggg  ataggccat  ggctggtccc ccaccatacc tcccctccac 1644
306 atcactgaca cagctgagct tgttatccat ctccccaaac tttctcttc  tttgtacttc 1704
308 ttgtcatccc cactcccagc ccctattcct ctatgtgaca gctggctagg accccctctgc 1764
310 cttcctcccc aatcctgact ggctcctagg gaaggggaag gctcctggag ggcagcccta 1824
312 cctctcccat gccctttgcc ctcctccctc gcctccagtg gaggctgagc tgaccctggg 1884
314 ctgctggagg ccagactggg ctgtagttag cttttcatcc ctaaagaagg ctttccctaa 1944
316 ggaaccatag aagagaggaa gaaaacaaag ggcatgtgtg agggaagctg cttgggtggg 2004
318 tgttagggct atgaaatctt ggatttgggg ctgaggggtg ggagggaggg cagagctctg 2064
320 cacactcaaa ggctaaactg gtgtcagtcc tttttttcctt tgttccaaat aaaagattaa 2124
322 accaaaaaaa aaaaaaaaaa a                                            2145
325 <210> SEQ ID NO: 4
326 <211> LENGTH: 441
327 <212> TYPE: PRT
328 <213> ORGANISM: Homo sapiens
330 <400> SEQUENCE: 4
331 Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 05/23/2000
PATENT APPLICATION: US/09/225,502A   TIME: 21:22:03

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05232000\I225502A.raw

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L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:806 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:806 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:806 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:806 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:806 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:833 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:833 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:833 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:833 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:851 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:851 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:851 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:851 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
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